

An In-place Framework for Exact and Approximate Shortest Unique Substring Queries ^{*}

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Abstract. We revisit the exact shortest unique substring (SUS) finding problem, and propose its approximate version where mismatches are allowed, due to its applications in subfields such as computational biology. We design a generic in-place framework that fits to solve both the exact and approximate k -mismatch SUS finding, using the minimum $2n$ memory words plus n bytes space, where n is the input string size. By using the in-place framework, we can find the exact and approximate k -mismatch SUS for every string position using a total of $O(n)$ and $O(n^2)$ time, respectively, regardless of the value of k . Our framework does not involve any compressed or succinct data structures and thus is practical and easy to implement.

Keywords: string pattern matching, shortest unique substring, in-place algorithms

1 Introduction

We consider a **string** $S[1..n]$, where each character $S[i]$ is drawn from an alphabet $\Sigma = \{1, 2, \dots, \sigma\}$. We say the character $S[i]$ **occupies** the string position i . A **substring** $S[i..j]$ of S represents $S[i]S[i+1] \dots S[j]$ if $1 \leq i \leq j \leq n$, and is an empty string if $i > j$. We call i the **start position** and j the **ending position** of $S[i..j]$. We say the substring $S[i..j]$ **covers** the k th position of S , if $i \leq k \leq j$. String $S[i'..j']$ is a **proper substring** of another string $S[i..j]$ if $i \leq i' \leq j' \leq j$ and $j' - i' < j - i$. The **length** of a non-empty substring $S[i..j]$, denoted as $|S[i..j]|$, is $j - i + 1$. We define the length of an empty string as zero.

The **Hamming distance** of two non-empty strings A and B of equal length, denoted as $H(A, B)$, is defined as the number of string positions where the characters differ. A substring $S[i..j]$ is **k -mismatch unique**, for some $k \geq 0$, if there does not exist another substring $S[i'..j']$, such that $i' \neq i$, $j - i = j' - i'$, and $H(S[i..j], S[i'..j']) \leq k$. A substring is a **k -mismatch repeat** if it is not k -mismatch unique.

Definition 1 (k -mismatch SUS). For a particular string position p in S and an integer k , $0 \leq k \leq n - 1$, the k -mismatch shortest unique substring (SUS) covering position p , denoted as SUS_p^k , is a k -mismatch unique substring $S[i..j]$, such that (1) $i \leq p \leq j$, and (2) there does not exist another k -mismatch unique substring $S[i'..j']$, such that $i' \leq p \leq j'$ and $j' - i' < j - i$.

We call 0-mismatch SUS as **exact SUS**, and the case $k > 0$ as **approximate SUS**.

For any k and p , SUS_p^k must exist, because at least the string S can be SUS_p^k , if none of its proper substrings is SUS_p^k . On the other hand, there might be multiple choices for SUS_p^k . For example, if $S = \text{abcb}$, SUS_2^0 can be either $S[1, 2] = \text{ab}$ or $S[2, 3] = \text{bc}$, and SUS_1^1 can be either $S[1..3] = \text{abc}$ or

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$S[2..4] = \text{bcb}$. Note that in Definition 1, we require $k < n$, because finding SUS_p^n is trivial: $SUS_p^n \equiv S$ for any string position p .

Problem (k -mismatch SUS finding). Given the string S , the value of $k \geq 0$, and two empty integer arrays A and B , we want to work in the place of S , A , and B , such that, in the end of computation: (1) S does not change. (2) Each $(A[i], B[i])$ pair saves the start and ending positions of the rightmost⁴ SUS_i^k , i.e., $S[A[i]..B[i]] = SUS_i^k$, using a total of $O(n)$ time for $k = 0$ and $O(n^2)$ time for any $k \geq 1$.

1.1 Prior work and our contribution

Exact SUS finding was proposed and studied recently by Pei et al. [7], due to its application in locating snippets in document search, event analysis, and bioinformatics, such as finding the distinctness between closely related organisms [3], polymerase chain reaction (PCR) primer design in molecular biology, genome mapability [2], and next-generation short reads sequencing [1]. The algorithm in [7] can find all exact SUS in $O(n^2)$ time using a suffix tree of $O(n)$ space. Following their proposal, there has been a sequence of improvements [8,5] for exact SUS finding, reducing the time cost from $O(n^2)$ to $O(n)$ and alleviating the underlying data structure from suffix tree to suffix array of $O(n)$ space. Hu et al. [4] proposed an RMQ (range minimum query) technique based indexing structure, which can be constructed in $O(n)$ time and space, such that any future exact SUS covering any interval of string positions can be answered in $O(1)$ time. In this work, we make the following contributions:

- We revisit the exact SUS finding problem and also propose its approximate version where mismatches are allowed, which significantly increases the difficulty as well as the usage of SUS finding in subfields such as bioinformatics, where approximate string matching is unavoidable due to genetic mutation and errors in biological experiments.
- We propose a generic in-place algorithmic framework that fits to solve both the exact and approximate k -mismatch SUS finding, using $2n$ words plus n bytes space. It is worth mentioning that $2n$ words plus n bytes is the minimum memory space needed to save those n calculated SUSes: (1) It needs 2 words to save each SUS by saving its start and ending positions (or one endpoint and its length) and there are n SUSes. (2) It needs another n bytes to save the original string S in order to output the actual content of any SUS of interest from queries. Note that all prior work [7,8,5,4] use $O(n)$ space but there is big leading constant hidden within the big-oh notation (see the experimental study in [5]).
- After the suffix array is constructed, all the computation in our solution happens in the place of two integer arrays, using non-trivial techniques. It is worth noting that our solution does not involve any compressed or succinct data structures, making our solution practical and easy to implement. Our preliminary experimental study shows that our solution for exact SUS finding is even faster than the fastest one among [7,8,5]⁵, in addition to a lot more space saving than them, enabling our solution to handle larger data sets. Due to page limit, we will deliver the details of our experimental study in the journal version of this paper.

2 Preparation

A **prefix** of S is a substring $S[1..i]$, $1 \leq i \leq n$. A **proper prefix** $S[1..i]$ is a prefix of S where $i < n$. A **suffix** of S is a substring $S[i..n]$, denoted as S_i , $1 \leq i \leq n$. S_i is a **proper suffix** of S , if $i > 1$.

⁴ Since any SUS may have multiple choices, it is our arbitrary decision to resolve the ties by picking the rightmost choice. However, our solution can also be easily modified to find the leftmost choice.

⁵ Note that the work of [4] studies a different problem and its computation is of the query-answer model, and thus is not comparable with [7,8,5] and ours.

For two strings A and B , we write $\mathbf{A} = \mathbf{B}$ (and say A is **equal** to B), if $|A| = |B|$ and $H(A, B) = 0$. We say A is lexicographically smaller than B , denoted as $\mathbf{A} < \mathbf{B}$, if (1) A is a proper prefix of B , or (2) $A[1] < B[1]$, or (3) there exists an integer $k > 1$ such that $A[i] = B[i]$ for all $1 \leq i \leq k-1$ but $A[k] < B[k]$.

The **suffix array** $SA[1..n]$ of the string S is a permutation of $\{1, 2, \dots, n\}$, such that for any i and j , $1 \leq i < j \leq n$, we have $S[SA[i]..n] < S[SA[j]..n]$. That is, $SA[i]$ is the start position of the i th smallest suffix in the lexicographic order. The **rank array** $RA[1..n]$ is the inverse of the suffix array, i.e., $RA[i] = j$ iff $SA[j] = i$. The **k -mismatch longest common prefix (LCP)** between two strings A and B , $k \geq 0$, denoted as $LCP^k(A, B)$, is the LCP of A and B within Hamming distance k . For example, if $A = abc$ and $B = acb$, then: $LCP^0(A, B)$ is $A[1] = B[1] = a$ and $|LCP^0(A, B)| = 1$; $LCP^1(A, B)$ is $A[1..2] = ab$ and $B[1, 2] = ac$ and $|LCP^1(A, B)| = 2$.

Definition 2 (k -mismatch LSUS). For a particular string position p in S and an integer k , $0 \leq k \leq n-1$, the k -mismatch left-bounded shortest unique substring (LSUS) starting at position p , denoted as $LSUS_p^k$, is a k -mismatch unique substring $S[p..j]$, such that either $p = j$ or any proper prefix of $S[p..j]$ is not k -mismatch unique.

We call 0-mismatch LSUS as **exact LSUS**, and the case $k > 0$ as **approximate LSUS**.

Observe that for any k , $LSUS_1^k = SUS_1^k$ always exists, because at least the whole string S can be $LSUS_1^k$. However, for any $k \geq 0$ and $p \geq 2$, $LSUS_p^k$ may not exist. For example, if $S = dabcabc$, none of $LSUS_i^0$ and $LSUS_j^1$ exists, for all $i \geq 5$, $j \geq 4$. It follows that some string positions may not be covered by any k -mismatch LSUS. For example, for the same string $S = dabcabc$, positions 6 and 7 are not covered by any exact or 1-mismatch LSUS. On the other hand, if any $LSUS_p^k$ does exist, there must be only one choice for $LSUS_p^k$, because $LSUS_p^k$ has its start position fixed on p and need to be as short as possible. Note that in Definition 2, we require $k < n$, because finding $LSUS_p^n$ is trivial as $LSUS_1^n \equiv S$ and $LSUS_p^n$ does not exist for all $p > 1$.

Definition 3 (k -mismatch SLS). For a particular string position p in S and an integer k , $0 \leq k \leq n-1$, we use SLS_p^k to denote the shortest k -mismatch LSUS covering position p .

We call 0-mismatch SLS as **exact SLS**, and the case $k > 0$ as **approximate SLS**.

SLS_p^k may not exist, since position p may not be covered by any k -mismatch LSUS at all. For example, if $S = dabcabc$, then none of SLS_p^0 and SLS_p^1 exists, for all $p \geq 6$. On the other hand, if SLS_p^k exists, there might be multiple choices for SLS_p^k . For example, if $S = abcbac$, SLS_2^0 can be either $LSUS_1^0 = S[1..2]$ or $LSUS_2^0 = S[2..3]$, and SLS_3^1 can be any one of $LSUS_1^1 = S[1..3]$, $LSUS_2^1 = S[2..4]$, and $LSUS_3^1 = S[3..5]$. Note that in Definition 3, we require $k < n$, because finding SLS_p^n is trivial as $SLS_p^n \equiv S$ for all p .

Lemma 1. For any k and p : (1) $LSUS_1^k$ always exists. (2) If $LSUS_p^k$ exists, then $LSUS_i^k$ exists, for all $i \leq p$. (3) If $LSUS_p^k$ does not exist, then none of $LSUS_i^k$ exists, for all $i \geq p$.

Proof. (1) $LSUS_1^k$ must exist, because at least the string S can be $LSUS_1^k$ if every proper prefix of S is a k -mismatch repeat. (2) If $LSUS_p^k$ exists, say $LSUS_p^k = S[p..q]$, $q \geq p$, then $LSUS_i^k$ exists for every $i \leq p$, because at least $S[i..q]$ is k -mismatch unique. (3) It is true, because otherwise we get a contradiction to the second statement in the lemma. \square

Lemma 2. For any k and p , $|LSUS_p^k| \geq |LSUS_{p-1}^k| - 1$, if $LSUS_p^k$ exists.

Proof. Suppose the k -mismatch substring $LSUS_p^k = S[p..q]$, for some $q \geq p$. Then, $S[p-1..q]$ is also k -mismatch unique. It follows immediately that, $|LSUS_{p-1}^k| \leq |S[p-1..q]| = 1 + |LSUS_p^k|$. \square

Lemma 3. For any k and p , SUS_p^k is either SLS_p^k or $S[i..p]$, for some i , $i + |LSUS_i^k| - 1 < p$. That is, SUS_p^k is either the shortest k -mismatch LSUS that covers position p , or a right extension (through position p) of a k -mismatch LSUS.

Proof. We know SUS_p^k must exist, because at least the string S can be SUS_p^k . Let's say $SUS_p^k = S[i..j]$, $i \leq p \leq j$. If $S[i..j]$ is neither $LSUS_i^k$ nor a right extension of $LSUS_i^k$, it means $S[i..j]$ is a proper prefix of $LSUS_i^k$ and thus is a k -mismatch repeat, which is a contradiction to the fact that $S[i..j] = SUS_p^k$ is k -mismatch unique. Therefore, $SUS_p^k = S[i..j]$ is either $LSUS_i^k$, or a right extension of $LSUS_i^k$ (clearly, $j \equiv p$ in this case). Further, if $SUS_p^k = S[i..j] = LSUS_i^k$, it is obvious that $LSUS_i^k$ must be the shortest k -mismatch LSUS covering position p , i.e., $SUS_p^k = SLS_p^k$. \square

For example, let $S = \text{dabcabc}$, then: (1) SUS_3^0 can be either $S[3..5] = LSUS_3^0$, or $S[1..3]$, which is a right extension of $LSUS_1^0 = S[1]$. (2) $SUS_5^0 = S[4..5] = LSUS_4^0$. (3) $SUS_6^0 = S[4..6]$, which is a right extension of $LSUS_4^0 = S[4..5]$. (4) $SUS_4^1 = S[3..5] = LSUS_3^1$. (5) $SUS_6^1 = S[3..6]$, which is a right extension of $LSUS_3^1$.

The next lemma further says that if SUS_p^k is an extension of an k -mismatch LSUS, SUS_p^k can be quickly obtained from SUS_{p-1}^k .

Lemma 4. For any k and p , if $SUS_p^k = S[i..p]$ and $i + |LSUS_i^k| - 1 < p$, i.e., SUS_p^k is a right extension (through position p) of $LSUS_i^k$, then the following must be true: (1) $p > 2$; (2) the rightmost character of SUS_{p-1}^k is $S[p-1]$; (3) $SUS_p^k = SUS_{p-1}^k S[p]$, the substring SUS_{p-1}^k appended by the character $S[p]$.

Proof. If SUS_p^k is a right extension (through position p) of a k -mismatch LSUS, it is certain that $p > 1$, because $SUS_1^k \equiv LSUS_1^k$, which always exists (Lemma 1).

Because SUS_p^k is a right extension (through position p) of a k -mismatch LSUS, we have $SUS_p^k = S[i..p]$ for some $i < p$, and $LSUS_i^k = S[i..j]$ for some $j < p$. We also know $S[i..p-1]$ is k -mismatch unique, because the k -mismatch unique substring $S[i..j]$ is a prefix of $S[i..p-1]$. Note that any substring starting from a position before i and covering position $p-1$ is longer than the k -mismatch unique substring $S[i..p-1]$, so SUS_{p-1}^k must be starting from a position between i and $p-1$, inclusive. Next, we show SUS_{p-1}^k actually must start at position i .

The fact that $SUS_p^k = S[i..p]$ implies $|LSUS_t^k| \geq |SUS_p^k| = p - i + 1$ for every $t = i+1, i+2, \dots, p$; otherwise, rather than $S[i..p]$, any one of these $LSUS_t^k$ whose size is smaller than $p - i + 1$ would be a better choice for SUS_p^k . That means, any k -mismatch unique substring starting from $t = i+1, i+2, \dots, p-1$ has a length at least $p - i + 1$. However, $|S[i..p-1]| = p - i < p - i + 1$ and $S[i..p-1]$ is k -mismatch unique already and covers position $p-1$ as well, so $S[i..p-1]$ is the only choice for SUS_{p-1}^k . This also means SUS_p^k is indeed the substring SUS_{p-1}^k appended by the character $S[p]$. \square

3 The High-Level Picture

In this section, we present an overview of our in-place framework for finding both the exact and approximate SUS. The framework is composed of three stages, where all computation happens in the place of three arrays, S , A , and B , each of size n . Arrays A and B are of integers, whereas array S always saves the input string. The following table summarizes the roles of A and B at different stages by showing their content at the end of each stage.

Stages	$A[i]$	$B[i]$
1	Used as temporary workspace during stage 1, but the content is useless for stages 2 and 3.	Ending position of $LSUS_i^k$, if $LSUS_i^k$ exists; otherwise, NIL.
2	The largest j , such that $LSUS_j^k$ is an SLS_i^k , if SLS_i^k exists; otherwise, NIL.	Ending position of $LSUS_i^k$, if $LSUS_i^k$ exists; otherwise, NIL.
3	Start position of the rightmost SUS_i^k	Ending position of the rightmost SUS_i^k

Stage 1 (Section 4). We take the array S that saves the input string as input to compute $LSUS_i^k$ for all i , in the place of A and B . At the end of the stage, each $B[i]$ saves the ending position of $LSUS_i^k$, if $LSUS_i^k$ exists. Since each existing $LSUS_i^k$ has its start position fixed at i , at the end of stage 1, each existing $LSUS_i^k = S[i..B[i]]$. For those non-existing k -mismatch LSUSes, we assign NIL to the corresponding B array elements. The time cost of this stage is $O(n)$ for exact LSUS finding ($k = 0$), and is $O(n^2)$ for approximate LSUS finding, for any $k \geq 1$.

Stage 2 (Section 5). Given the array B (i.e., the k -mismatch LSUS array of S) from stage 1, we compute the rightmost SLS_i^k , the rightmost shortest LSUS covering position i , for all i , in the place of A and B . At the end of stage 2, each $A[i]$ saves the largest j , such that $LSUS_j^k$ is an SLS_i^k , i.e., the rightmost $SLS_i^k = S[A[i]..B[A[i]]]$, if SLS_i^k exists; otherwise, we assign $A[i] = \text{NIL}$. Array B does not change during stage 2. The time cost of this stage is $O(n)$, for any $k \geq 0$.

Stage 3 (Section 6). Given A and B from stage 2, we compute SUS_i^k , for all i , in the place of A and B . At the end of stage 3, each $(A[i], B[i])$ pair saves the start and ending positions of the rightmost SUS_i^k , i.e., $SUS_i^k = S[A[i]..B[i]]$. The time cost of this stage is $O(n)$, for any $k \geq 0$.

Algorithms 1, 2, 3, and 4 in the appendix give the pseudocode of the in-place procedures that we will describe in Sections 4.1, 4.2, 5, and 6, respectively.

4 Finding k -mismatch LSUS

The goal of this section is that, given the input string S and two integer arrays A and B , we want to work in the place of A and B , such that $B[i]$ saves the ending position of $LSUS_i^k$ for all existing $LSUS_i^k$; otherwise, $B[i]$ is assigned NIL. We take different approaches in finding the exact LSUS ($k = 0$) and approximate LSUS ($k \geq 1$).

4.1 Finding exact LSUS ($k = 0$)

Lemma 5 (Lemma 7.1 in [6]). *Given the string S of size n , drawn from an alphabet of size σ , we can construct the suffix array SA of S in $O(n)$ time, using $n + \sigma$ words plus n bytes, where the space of n bytes saves S , the space of n words saves SA , and the extra space of σ words is used as the workspace for the run of the SA construction algorithm.*

Given the input string S , we first use the $O(n)$ -time suffix array construction algorithm from [6] to create the SA of S , where the array A is used to save the SA and the array B is used as the workspace. Note that $\sigma \leq n$ is always true, because otherwise we will prune from the alphabet those characters that do not appear in the string. After SA (saved in A) is constructed, we can easily spend another $O(n)$ time to create the rank array RA of S (saved in B): $RA[SA[i]] \leftarrow i$ (i.e., $B[A[i]] \leftarrow i$), for all i . Next, we use and work in the place of A (i.e., SA) and B (i.e., RA) to compute the ending position of each existing $LSUS_i^0$ and save the result in $B[i]$, using another $O(n)$ time.

Definition 4.

$$x_i = \begin{cases} |LCP^0(S[i..n], S[SA[RA[i] - 1]..n])|, & \text{if } RA[i] > 1 \\ 0, & \text{otherwise} \end{cases}$$

$$y_i = \begin{cases} |LCP^0(S[i..n], S[SA[RA[i] + 1]..n])|, & \text{if } RA[i] < n \\ 0, & \text{otherwise} \end{cases}$$

That is, x_i (y_i , resp.) is the length of the longest common prefix of $S[i..n]$ and its lexicographically preceding (succeeding, resp.) suffix, if the preceding (succeeding, resp.) suffix exists.

Fact 1 For every string position i , $1 \leq i \leq n$:

$$LSUS_i^0 = \begin{cases} S[i..i + \max\{x_i, y_i\}], & \text{if } i + \max\{x_i, y_i\} \leq n \\ \text{not existing}, & \text{otherwise.} \end{cases}$$

First, observe that in the sequence of x_i 's, if $x_i > 0$, then $x_{i+1} \geq x_i - 1$ must be true, because at least $S[SA[RA[i] - 1] + 1..n]$ can be the lexicographically preceding suffix of $S[i + 1..n]$, and they share the leading $x_i - 1$ characters. That means, when we compute x_{i+1} , we can skip over the comparisons of the first $x_i - 1$ pair of characters between $S[i + 1..n]$ and its lexicographically preceding suffix. It follows that, given the SA and RA of S and using the above observation, we can compute the sequence of x_i 's in $O(n)$ time. Using the similar observation, we can compute the sequence of y_i 's in $O(n)$ time, provided that S and its SA and RA are given.

Second, since we can compute the sequences of x_i 's and y_i 's in parallel (i.e., compute the sequence of (x_i, y_i) pairs), we can use Fact 1 to compute the sequence of $LSUS_i^0$ in $O(n)$ time. Further, since $RA[i]$ is used only for retrieving the lexicographically preceding and succeeding suffixes of $S[i..n]$ when we compute the pair (x_i, y_i) , we can save each computed $LSUS_i^0$ (indeed, $i + \max\{x_i, y_i\}$, the ending position of $LSUS_i^0$) in the place of $RA[i]$ (i.e., $B[i]$). In the case $i + \max\{x_i, y_i\} > n$, meaning $LSUS_i^0$ does not exist, we will assign NIL to $RA[j]$ (i.e., $B[j]$) for all $j \geq i$ (Lemma 1). The overall time cost for computing the sequence of $LSUS_i^0$ is thus $O(n)$, yielding the following lemma.

Lemma 6. Given the character array S of size n that saves the input string, and the integer arrays A and B , each of size n , we can work in the place of S , A , and B , using $O(n)$ time, such that at the end of the computation, S does not change, $B[i]$ saves the ending of position of $LSUS_i^0$, if $LSUS_i^0$ exists (otherwise, $B[i] = \text{NIL}$).

4.2 Finding approximate LSUS ($k \geq 1$)

Definition 5. For a particular string position p in S and an integer k , $0 \leq k \leq n - 1$, the k -mismatch left-bounded longest repeat (LLR) starting at position p , denoted as LLR_p^k , is a k -mismatch repeat $S[p..j]$, such that either $j = n$ or $S[p..j + 1]$ is k -mismatch unique.

Fact 2 (1) If $|LLR_p^k| < n - p + 1$, i.e., the ending position of LLR_p^k is less than n , then $LSUS_p^k = S[p..p + |LLR_p^k|]$, the substring of LLR_p^k appended by the character following LLR_p^k . (2) Otherwise, $LSUS_p^k$ does not exist.

Our high-level strategy for finding $LSUS_i^k$ for all i is as follows. We first find LLR_i^k for all i . Then we use Fact 2 to find each $LSUS_i^k$ from LLR_i^k : If LLR_i^k does not end on position n , we will extend it for one more character on its right side and make the extension to be $LSUS_i^k$; otherwise, LLR_i^k does not exist. Next, we explain how to find LLR_i^k , for all i .

Clearly, $|LLR_i^k| = \max\{|LCP^k(S_i, S_j)|, j \neq i\}$, for all i . The way we calculate $|LLR_i^k|$ for all i is simply to let every pair of two distinct suffixes to be compared with each other. In order to do so, we work over $n - 1$ phases, named as \mathcal{P}_1 through \mathcal{P}_{n-1} . On a particular phase \mathcal{P}_δ , we compare suffixes S_i and $S_{i-\delta}$ for all $i = n, n-1, \dots, \delta+1$. Obviously, over these $n - 1$ phases, every pair of distinct suffixes have been compared with each other exactly once. Over these $n - 1$ phases, we simply record in $B[i]$, which is initialized to be 0, the length of the longest k -mismatch LCP that each suffix S_i has seen when compared with any other suffixes. Next, we explain the details of a particular phase \mathcal{P}_δ .

On a particular phase \mathcal{P}_δ , $1 \leq \delta \leq n-1$, we compare suffixes S_i and $S_{i-\delta}$ for all $i = n, n-1, \dots, \delta+1$. When we compare S_i and $S_{i-\delta}$, we save in $A[1..k+1]$, which is initialized to be empty at the beginning of each phase, the leftmost mismatched $k+1$ positions in S_i . We will see later how to update $A[1..k+1]$ efficiently over the progress of a particular phase and use it to update the B array.

We treat $A[1..k+1]$ as a circular array, i.e., $i-1 = k+1$ when $i = 1$, and $i+1 = 1$ when $i = k+1$. Let size , which is initialized to be 0 at the beginning of each phase, denote the number of mismatched positions being saved in $A[1..k+1]$ so far in \mathcal{P}_δ . We can describe the work of phase \mathcal{P}_δ , inductively, as follows.

1. We compare S_n and $S_{n-\delta}$ by only comparing $S[n]$ and $S[n-\delta]$, since $S_n = S[n]$.
 - (a) If $S[n] \neq S[n-\delta]$: Save n in any position in $A[1..k+1]$; $\text{size} \leftarrow 1$.
 - (b) $B[n] \leftarrow \max\{B[n], 1\}$; $B[n-\delta] \leftarrow \max\{B[n-\delta], 1\}$.
2. Suppose we have finished the comparison between the suffixes S_{i+1} and $S_{i+1-\delta}$, for some i , $\delta+1 \leq i \leq n-1$. The leftmost $k+1$ mismatched positions (if existing) between them have been saved in the circular array $A[1..k+1]$. Let $A[\text{cursor}]$ be the element that is saving the first mismatched position (if existing) between the two suffixes.
3. Next, we compare the suffixes S_i and $S_{i-\delta}$ by only comparing $S[i]$ and $S[i-\delta]$, since S_{i+1} and $S_{i+1-\delta}$ have been compared. Remind that $\text{cursor} - 1$ below is in its cyclic manner.
 - (a) If $S[i] \neq S[i-\delta]$: $\text{cursor} \leftarrow \text{cursor} - 1$; Save i in $A[\text{cursor}]$ and overwrite the old content in $A[\text{cursor}]$ if there is; $\text{size} \leftarrow \min\{\text{size} + 1, k+1\}$.
 - (b) If $\text{size} < k+1$: $B[i] \leftarrow \max\{B[i], n-i+1\}$; $B[i-\delta] \leftarrow \max\{B[i-\delta], n-i+1\}$.
 - (c) Else: $B[i] \leftarrow \max\{B[i], A[\text{cursor}-1]-i\}$; $B[i-\delta] \leftarrow \max\{B[i-\delta], A[\text{cursor}-1]-i\}$. Note that $A[\text{cursor}-1]$ is saving the $(k+1)$ th mismatched position between S_i and $S_{i-\delta}$.

After the computation of all LLR_i^k is finished, using the above $n-1$ phases, each $B[i]$ is saving $|LLR_i^k|$. Next, we can use Fact 2 to convert each LLR_i^k to $LSUS_i^k$ by simply checking each $B[i]$: If $i+B[i]-1 < n$, i.e., LLR_i^k does not end on position n , then we assign $B[i] = i+B[i]$, the ending position of $LSUS_i^k$; otherwise, we assign $B[i] = \text{NIL}$, meaning $LSUS_i^k$ does not exist.

The computation of all LLR_i^k takes $n-1$ phases and each phase clearly has no more than n comparisons, giving a total of $O(n^2)$ time cost. The procedure of converting each LLR_i^k to $LSUS_i^k$ spends another $O(n)$ time. Altogether, we get an $O(n^2)$ -time in-place procedure for finding approximate LSUS, for any $k \geq 1$.

Lemma 7. *Given the character array S of size n that saves the input string, the integer arrays A and B , each of size n , and the value of integer $k \geq 1$, we can work in the place of S , A , and B , using $O(n^2)$ time, such that at the end of the computation, S does not change, $B[i]$ saves the ending of position of $LSUS_i^k$, i.e., $LSUS_i^k = S[i..B[i]]$, if $LSUS_i^k$ exists; otherwise, $B[i] = \text{NIL}$.*

5 Finding k -mismatch SLS

Now we are given the array B , where each $B[i]$ saves the ending position of $LSUS_i^k$ if $LSUS_i^k$ exists and NIL otherwise. In this section, we want to work in the place of A and B , such that in the end of computation: $A[i]$ saves j , such that $LSUS_j^k$ is the rightmost SLS_i^k , if such j exists; otherwise, $A[i] = \text{NIL}$. That means, in the end of this section, the rightmost $SLS_i^k = S[A[i]..B[A[i]]]$, if SLS_i^k exists; otherwise, $A[i] = B[i] = \text{NIL}$.

Recall that some k -mismatch LSUS may not exist and some positions may not be covered by any k -mismatch LSUS (see the examples after Definition 2). Further, due to Lemmas 1 and 2, we know such positions that are not covered by any k -mismatch LSUS must comprise a continuous chunk on the right end of string S .

Definition 6. Let $LSUS_r^k$, $1 \leq r \leq n$, be the rightmost existing k -mismatch LSUS of the input string S . Let z , $1 \leq z \leq n$, be the rightmost string position that is covered by any k -mismatch LSUS of the string S .

Again, due to Lemmas 1 and 2, it is trivial to find the values of r and z in $O(n)$ time: scan array B (i.e. LSUS array) from right to left, and stop when seeing the first non-NIL B array element, which is exactly $B[r]$, then $z = B[r]$. If $z < n$, we can then simply set $A[i] = \text{NIL}$ for all $i > z$. Recall that $B[i] = \text{NIL}$ already for all $i > r$ from stage 1. In the rest of this section, we only need to work with the two subarrays $A[1..z]$ and $B[1..z]$, wanting to make $A[i]$ to be the start position of the rightmost SLS_i^k , for all $i \leq z$.

Let $B[1..z]$ and an integer r , $1 \leq r \leq z$, be the input, where (1) $B[1..r]$ is of monotonically nondecreasing integers (Lemma 2), with $i \leq B[i]$, (2) $B[r+1..z]$ are all NIL, if $r < z$, and (3) $B[r] = z$.

We can use each $B[i]$, $i \leq r$, as a compact representation of the interval $I_i = (i, B[i])$. Let $\mathcal{I} = \{ I_i \mid i \in [1..r] \}$, and $\ell_i = |B[i] - i + 1|$ be the length of I_i . Let $A[1..z]$ be an output array such that $A[j] = i$, where I_i is the rightmost shortest interval in \mathcal{I} that covers j .

To illustrate the ideas and concepts that we will present in the rest of this section, let us use the following as a running example, where $r = 9$, $z = 15$, and $n = 17$ (we add $(0, B[0]) = (0, 0)$ as a sentinel).

i	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17
$B[i]$	0	3	4	7	8	10	10	10	11	15	—	—	—	—	—	—	—	—
ℓ_i	0	3	3	5	5	6	5	4	4	7	—	—	—	—	—	—	—	—
$\text{pred}[i]$	—	—	—	2	2	4	2	2	2	8	—	—	—	—	—	—	—	—
t_i	—	1	2	5	5	9	6	7	8	12	—	—	—	—	—	—	—	—
$\max t_i^{-1}$	—	1	2	—	—	4	6	7	8	5	—	—	9	—	—	—	—	—
$A[i]$	—	1	2	2	2	4	6	7	8	8	8	8	9	9	9	9	—	—

Definition 7. For an interval I_i , we define the effective covering region with respect to the previous intervals $\mathcal{I}_{<i} = \{ I_k \mid k < i \}$ to be $[t_i, B[i]]$ where

$$t_i = \max \left\{ i, \max \{ B[k] + 1 \mid I_k \text{ is shorter than } I_i, k < i \} \right\}.$$

We call t_i the starting point of the effective covering region of I_i .

The effective covering region of I_i is exactly those regions that would set I_i as the answer, provided that all the intervals $I_{<i}$ before I_i are present, and all the intervals $I_{>i} = \{ I_k \mid k > i \}$ are absent.

We next define t_i^{-1} as a list⁶, such that $j \in t_i^{-1}$ if and only if $t_j = i$. Observe that since $t_i \geq i$ by definition, any value j in t_i^{-1} must have $j \leq i$, and the effective region of I_j must cover i .

⁶ In actual run, t_i^{-1} saves the largest number in that list, as we will see more clearly later.

Lemma 8. For $i = 1, 2, \dots, z$:

$$A[i] = \max \bigcup_{k=1}^i t_k^{-1} = \max \{ A[i-1], \max t_i^{-1} \}.$$

Proof. Let $j = \max \bigcup_{k=1}^i t_k^{-1}$. This means that for the effective region of any I_h , with $h > j$, none of them covers i . Next, observe that I_j must cover i ; otherwise, for all the intervals I_h with $h < j$, we have $B[h] \leq B[j] < i$, so that none of them can cover i , and thus a contradiction occurs. Finally, we show that for those $h < j$, I_h can be pruned by I_j , thus implying that $A[i] = j$ is a correct answer.

Consider all those h with $h < j$:

1. If I_h is longer than I_j , I_h can be pruned away directly.
2. Else, if I_h and I_j have equal length, I_h can be pruned away also, regardless of its coverage on i , since we pick the rightmost shortest interval that covers i .
3. Else, h must appear in $\bigcup_{k=1}^i t_k^{-1}$. By the definition of t_j , we have $B[h] < t_j \leq i$; thus, I_h does not cover i , and can be pruned away.

Thus, the first equality in the lemma follows, while the second equality in the lemma is trivial once we have the first equality. \square

Lemma 9. Suppose that all t_i , $1 \leq i \leq r$, can be generated incrementally in $O(n)$ time. Then, we can obtain all $\max t_i^{-1}$, $1 \leq i \leq z$, in $O(n)$ time.

Proof. We examine each t_i , $i = 1, 2, \dots, r$, and write i at entry $t_i = j$ of the t^{-1} array; if such an entry contains a value i' already, we simply overwrite i' with the latter i . \square

Indeed, we may scan t_i from right to left, i.e., $i = r, r-1, \dots, 1$, and update $\max t_i^{-1}$ as we proceed. Firstly, if $t_i > i$, we set $t_i^{-1} = \text{undefined}$. Else, let $j = t_i$ (whose value is at least i), and we check if t_j^{-1} is defined: If not, simply set $t_j^{-1} = i$; otherwise, no update is needed.

The advantage of the ‘right-to-left’ approach is that we can construct t_i^{-1} in-place, by re-using the memory space of t_i . To see why it is so, by the time we need to update a certain entry $j = t_i$ at step i , the information t_j has been used (and will never be used), so that we can safely overwrite the original entry, storing t_j , to store t_j^{-1} instead. This gives the following corollary.

Corollary 1. Suppose that all t_i ’s are generated, and are stored in a certain array $A[1..z]$. Then, we can obtain $\max t_i^{-1}$ for all i ’s, in-place, by storing the results in the same array $A[1..z]$; the time cost is $O(n)$.

Our goal is to make our algorithm in-place. Suppose that we can have in-place incremental generation of t_i . Then, by the above lemma, we may store $\max t_i^{-1}$ temporarily at $A[i]$; afterwards, by the second equality of Lemma 8, we can compute the correct output A by a simple scan of A from left to right.

Thus, to make the whole process in-place, it remains to show how t_i can be computed in $O(n)$ time, in-place. For this, we define $\text{pred}[i]$ to be the largest j (if it exists) such that $j < i$ and length of I_j is shorter than I_i . It is easy to check that if $\text{pred}[i] = j$ is defined, then $t_i = \max \{ B[j] + 1, i \}$ (and $t_i = i$ otherwise).⁷ Moreover, $\text{pred}[i]$ for all i ’s can be computed incrementally, with a way analogous to the construction of the failure function in KMP algorithm: we check $\text{pred}[i-1]$, $\text{pred}[\text{pred}[i-1]]$, $\text{pred}[\text{pred}[\text{pred}[i-1]]]$,

⁷ For each $j' < j$, if $I_{j'}$ covers i , I_j would also cover i ; in such a case, $B[j] + 1 \geq B[j'] + 1$. For each $j' \in [\text{pred}[i], i-1]$, $I_{j'}$ is longer than I_i .

and so on, until we obtain j in the process such that I_j is shorter than I_i , and set $\text{pred}[i] := j$.⁸ If such j does not exist, we set $\text{pred}[i] = \text{NIL}$. The running time is bounded by $O(n)$.

This gives the following $O(n)$ -time in-place algorithm (where B is read-only):

1. Compute $\text{pred}[i]$, $i = 1, 2, \dots, r$, and store this in $A[i]$. Note that this step requires the length information of the intervals of I_i , which can be obtained in $O(1)$ time, on the fly, from $B[i]$.
2. Scan $A[1..r]$ (i.e., pred) incrementally, and obtain t_i from the above discussion. The value of t_i is stored in $A[i]$. Note that this step requires the access to the original B .
3. Scan $A[1..r]$ (i.e., t_i) from right to left, and obtain $\max t_i^{-1}$ decrementally (stored in $A[i]$) by Corollary 1.
4. Scan $A[1..z]$ (i.e., $\max t_i^{-1}$) incrementally ($i = 1, 2, \dots, z$), and obtain the desired $A[i]$ by the second equality in Lemma 8.

Lemma 10. *Given the integer array A and B , each of size n , where each $B[i]$ saves the ending position of $LSUS_i^k$, if $LSUS_i^k$ exists and NIL otherwise, we can work in the place of array A and B , using $O(n)$ time, such that, in the end of computation, array B does not change, and $A[i]$ saves j , where $LSUS_j^k$ is the rightmost SLS_i^k , if such j exists; otherwise, $A[i] = \text{NIL}$. That is, $SLS_i^k = S[A[i]..B[A[i]]]$, if SLS_i^k exists; otherwise, $A[i] = B[i] = \text{NIL}$.*

6 Finding k -mismatch SUS

Now we have array A , where $A[i] = j$, such that $LSUS_j^k$ is the rightmost SLS_i^k , if position i is covered by any k -mismatch LSUS; otherwise, $A[i] = \text{NIL}$. Note that $A[i] = j$ is recording the start position of the rightmost SLS_i^k already, because $LSUS_j^k$ starts on position j . We also have array B , where $B[i] = i + |LSUS_i^k| - 1$, the ending position of $LSUS_i^k$, if $LSUS_i^k$ exists; otherwise, $B[i] = \text{NIL}$.

Step I. We want to transform A and B , such that each $(A[i], B[i])$ pair saves the start and ending positions of SLS_i^k , if SLS_i^k exists; otherwise, we set $(A[i], B[i]) = (\text{NIL}, \text{NIL})$. Since each $A[i]$ is already recording the start position of SLS_i^k already, as we have explained at the beginning of this section, we only need to make changes to array B . We first set $B[i] = \text{NIL}$ for all $i > z$ (Definition 6). Then, we scan array B from right to left, starting from position z through 1, and set each $B[i] = B[A[i]]$, the ending position of the rightmost SLS_i^k . Because the leftmost position that any existing $LSUS_i^k$ can cover is position i , we know $A[i] \leq i$ and we no longer need $B[i]$ (i.e., the information of $LSUS_i^k$) after SLS_i is computed. Therefore, it is safe to record SLS_i^k by overwriting $B[i]$ by $B[A[i]]$ (i.e., the ending position of SLS_i^k), in this right-to-left scan.

Step II. We use arrays A and B to calculate SUS_i^k for each i and save the result in the place of A and B , i.e., each $(A[i], B[i])$ pair saves the start and ending position of SUS_i^k . Because of Lemma 3 and 4, we can use arrays A and B to compute each SUS_i^k inductively, as follows:

1. $SUS_1^k = LSUS_1^k = SLS_1^k = S[A[1]..B[1]]$.
2. For $i = 2, 3, \dots, n$, we compute SUS_i^k :
 - (a) If $(A[i], B[i]) = (\text{NIL}, \text{NIL})$, meaning SLS_i^k does not exist, we set SUS_i^k to be SUS_{i-1}^k appended by the character $S[i]$, i.e., $SUS_i^k = S[A[i-1]..B[i-1]+1]$, and save SUS_i^k by setting $(A[i], B[i]) = (A[i-1], B[i-1]+1)$;

⁸ Intuitively, pred defines the shortcuts so that we can skip some intervals in $I_{<i}$ to compute t_i .

- (b) Else, if SUS_{i-1}^k ends at position $i - 1$ and $SUS_{i-1}^k S[i] = S[A[i - 1]..B[i - 1] + 1]$ is shorter than $SLS_i^k = S[A[i]..B[i]]$, we set $(A[i], B[i]) = (A[i - 1], B[i - 1] + 1)$;
- (c) Else, $SUS_i^k = SLS_i^k$ and thus we leave $A[i]$ and $B[i]$ unchanged.

Lemma 11. *Given arrays A and B :*

- $A[i] = j$, such that $LSUS_j^k$ is the rightmost SLS_i^k , if SLS_i^k exists; otherwise, $A[i] = \text{NIL}$;
- $B[i] = i + |LSUS_i^k| - 1$, the ending position of $LSUS_i^k$, if $LSUS_i^k$ exists; otherwise, $B[i] = \text{NIL}$.

we can work in the place of A and B , using $O(n)$ time, such that, in the end of computation, each $(A[i], B[i])$ saves the start and ending positions of SUS_i^k , i.e., $SUS_i^k = S[A[i]..B[i]]$, $i = 1, 2, \dots, n$.

By concatenating the claims in Lemmas 6, 7, 10, and 11, we get the final result.

Theorem 1. *Given the array S of size n that saves the input string, two empty integer arrays A and B , each of size n , and the value of integer $k \geq 0$, we can work in the place of arrays S , A , and B , using a total of $O(n)$ time for $k = 0$ and $O(n^2)$ time for any $k \geq 1$, such that in the end of computation, S does not change, each $(A[i], B[i])$ pair represents the start and ending positions of the rightmost SUS_i^k , i.e., $SUS_i^k = S[A[i]..B[i]]$.*

7 Conclusion

In this paper, we revisited the exact SUS finding problem, and proposed its approximate version where mismatches are allowed, and thus significantly extended the usage of SUS finding in subfields such as computational biology. We designed a generic in-place algorithmic framework that uses the minimum $2n$ words plus n bytes space and can fit to find both exact and approximate k -mismatch SUS, with $O(n)$ and $O(n^2)$ time complexities, respectively, regardless of the value of any $k \geq 1$. An urgent future work will be researching for a faster (and still practical) in-place algorithm for finding approximate LSUS to replace the current algorithm discussed in Section 4.2. Such new algorithm will lead to an overall faster in-place solution for approximate SUS finding.

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Appendix

Algorithm 1: Finding exact LSUS

Input: String S and integer arrays A and B , each of size n .

Output: S does not change. $B[i]$ = ending position of $LSUS_i^0$, if $LSUS_i^0$ exists; otherwise, $B[i] = \text{NIL}$.

```

1 Create the  $SA$  of  $S$  using the suffix array construction algorithm from [6], where array  $A$  is used to save the resulting  $SA$ 
  and  $B$  is used as the workspace for the run of the algorithm.

  /* Create the  $RA$  of  $S$  and save the result in the array  $B$ . */
2 for  $i = 1 \dots n$  do  $RA[SA[i]] \leftarrow i$ ;           // i.e.,  $SA = A$ ,  $RA = B$ , and  $B[A[i]] \leftarrow i$ .

  /* From here on,  $A$  and  $SA$  are the same physical array.  $B$ ,  $RA$ , and  $LSUS$  are the
  same physical array. */

3  $x \leftarrow 0$ ;  $y \leftarrow 0$ ;
4 for  $i = 1, 2, \dots, n$  do
5   if  $RA[i] > 1$  then
6      $j \leftarrow SA[RA[i] - 1]$ ;
7     /* Calculate the length of the 0-mismatch LCP between  $S[i..n]$  and its
       lexicographically preceding suffix. */
8     while  $S[i + x] = S[j + x]$  do  $x \leftarrow x + 1$ ;
9   else  $x \leftarrow 0$ ;
10  if  $RA[i] < n$  then
11     $j \leftarrow SA[RA[i] + 1]$ ;
12    /* Calculate the length of the 0-mismatch LCP between  $S[i..n]$  and its
       lexicographically succeeding suffix. */
13    while  $S[i + y] = S[j + y]$  do  $y \leftarrow y + 1$ ;
14  else  $y \leftarrow 0$ ;
15  if  $i + \max\{x, y\} \leq n$  then  $LSUS[i] \leftarrow i + \max\{x, y\}$ ;           // ending position of  $|LSUS_i|$ 
16  else //  $LSUS_i$  does not exist. Early stop.
17    for  $j = i \dots n$  do  $LSUS[j] \leftarrow \text{NIL}$ ;
18    Break;
19  if  $x > 0$  then  $x \leftarrow x - 1$ ;
20  if  $y > 0$  then  $y \leftarrow y - 1$ ;

```

Algorithm 2: Finding approximate LSUS

Input: String S and integer arrays A and B , each of size n , the value of $k \geq 1$.

Output: S does not change. $B[i]$ = ending position of $LSUS_i^k$, if $LSUS_i^0$ exists; otherwise, $B[i] = \text{NIL}$.

```
1 for  $i = 1 \dots n$  do  $B[i] \leftarrow 0$ ; // Initialization
/* We use  $A[1 \dots k+1]$  as a circular array to save the  $k+1$  most recently found
   mismatched positions. */
2  $capacity \leftarrow k+1$ ; // The capacity of the circular array that records at most  $k+1$ 
   mismatched positions.
3  $cursor \leftarrow 1$ ; // The index of the circular array position that is saving the most
   recently founded mismatched position. It can be initialized to be any value from
    $\{1, 2, \dots, capacity\}$ .
4 for  $\delta = 1 \dots n-1$  do //  $n-1$  phases
5    $size \leftarrow 0$ ; // The number of recorded mismatched positions in the circular array in
   the current phase.
6   for  $i = n$  down to  $\delta+1$  do
7     /* Comparing suffixes  $S_i$  and  $S_{i-\delta}$  by comparing their leading characters, as
       their remaining characters have been compared in previous steps of this
       phase. */
8     if  $S[i] \neq S[i-\delta]$  then
9        $cursor \leftarrow ((cursor - 2 + capacity) \bmod capacity) + 1$ ; // We use 1-based indexing.
10       $A[cursor] \leftarrow i$ ;
11       $size \leftarrow \min(size + 1, capacity)$ ;
12      if  $size < capacity$  then
13         $B[i] \leftarrow \max(B[i], n - i + 1)$ ; //  $= size - i + 1$ 
14         $B[i - \delta] \leftarrow \max(B[i - \delta], n - i + 1)$ ;
15      else
16         $B[i] \leftarrow \max(B[i], A[((cursor - 1 + k) \bmod capacity) + 1] - i)$ ; // We use 1-based
        indexing.
17         $B[i - \delta] \leftarrow \max(B[i - \delta], A[((cursor - 1 + k) \bmod capacity) + 1] - i)$ ;
18 for  $i = 1 \dots n$  do
19   if  $B[i] = size - i + 1$  then  $B[i] \leftarrow \text{NIL}$ ; //  $LSUS_i^k$  does not exist.
   else  $B[i] \leftarrow i + B[i]$ ; // The ending position of  $LSUS_i^k$ .
```

Algorithm 3: Finding SLS (exact or approximate)

Input: Integer arrays A and B , each of size n . Each $B[i]$ saves the ending position of $LSUS_i^k$, if $LSUS_i^k$ exists; NIL , otherwise.

Output: Array B does not change. Each $A[i] = j$, such that $LSUS_j^k$ is the rightmost SLS_i^k , if SLS_i^k exists; otherwise, $A[i] = NIL$.

```

/* Find the index of the rightmost existing  $k$ -mismatch LSUS. */
1 for  $r = n$  down to 1 do if  $B[r] \neq NIL$  then break;

/* Compute the  $pred$  array, using the memory space of  $A$  array.  $pred[i]$  is the largest
 $j$ , such that  $j < i$  and  $|LSUS_j^k| < |LSUS_i^k|$ , if such  $j$  exists; otherwise  $pred[i] = NIL$ .
If  $LSUS_i^k$  does not exist,  $pred[i] = NIL$  also. From here on,  $pred$  and  $A$  are the same
physical array. */
2 if  $r < n$  then for  $i = r+1 \dots n$  do  $pred[i] \leftarrow NIL$ ; // Positions that do not have  $k$ -mismatch LSUS
3  $pred[1] \leftarrow NIL$ ;
4 for  $i = 2 \dots r$  do
5    $\ell_i \leftarrow B[i] - i + 1$ ; //  $|LSUS_i^k|$ 
6    $j \leftarrow i - 1$ ;
7   while  $pred[j] \neq NIL$  and  $B[j] - j + 1 \geq \ell_i$  do  $j \leftarrow pred[j]$ ;
8   if  $B[j] - j + 1 < \ell_i$  then  $pred[i] \leftarrow j$ ; else  $pred[i] \leftarrow NIL$ ;

/* Compute the  $t$  array, using the memory space of  $A$  array.  $t[i]$  is the start
position of the effective region of  $LSUS_i^k$ , if  $LSUS_i^k$  exists;  $NIL$ , otherwise.
From here on,  $t$  and  $A$  are the same physical array. */
9 for  $i = 1 \dots r$  do
10  if  $pred[i] = NIL$  then  $t[i] \leftarrow i$ ; else  $t[i] \leftarrow \max(B[pred[i]] + 1, i)$ ;

/* Compute the  $t^{-1}$  array, using the memory space of array  $A$ .  $t^{-1}[i]$  is the largest
 $j$ , such that the effective region of  $LSUS_j^k$  starts on position  $i$ , if such  $j$ 
exists; otherwise,  $NIL$ . From here on,  $t^{-1}$  and  $A$  are the same physical array. */
11 for  $i = r$  down to 1 do
12  if  $t^{-1}[t[i]] = NIL$  then  $t^{-1}[t[i]] \leftarrow i$ ;
13  if  $i < t[i]$  then  $t^{-1}[i] \leftarrow NIL$ ; // Enable us to update this place in the future when
    needed.

/* Compute  $SLS$  array using the memory space of array  $A$ .  $SLS[i] = j$ , such that  $LSUS_j^k$ 
is the rightmost  $SLS_i^k$ , if  $SLS_i^k$  exists;  $NIL$ , otherwise. From here on,  $SLS$  and  $A$ 
are the same physical array. */
14  $SLS[1] \leftarrow 1$ ;
15 for  $i = 2 \dots B[r]$  do  $SLS[i] \leftarrow \max(SLS[i-1], t^{-1}[i])$ ;

```

Algorithm 4: Finding SUS (exact or approximate)

Input: Integer arrays A and B , each of size n . (1) $A[i] = j$, such that $LSUS_j^k$ is the rightmost SLS_i^k , if SLS_i^k exists; otherwise, $A[i] = \text{NIL}$. (2) $B[i]$ is the ending position of $LSUS_i^k$, if $LSUS_i^k$ exists; otherwise, $B[i] = \text{NIL}$.

Output: Each $(A[i], B[i])$ pair represents the start and ending positions of SUS_i^k .

```
1 for  $i = n$  down to 1 do
2   if  $B[i] \neq \text{NIL}$  then
3      $z \leftarrow i + B[i] - 1$ ;    // The rightmost position covered by at least one  $k$ -mismatch
4      $\text{LSUS}$ .
5   break;
6 if  $z < n$  then
7   for  $i = z + 1 \dots n$  do
8      $B[i] \leftarrow \text{NIL}$ ;          // Positions not covered by any  $k$ -mismatch  $\text{LSUS}$ .
9 for  $i = z$  down to 1 do
10    $B[i] \leftarrow B[A[i]]$ ;      // The ending position of  $SLS_i^k$ .

/* By this point,  $S[A[i]..B[i]] = SLS_i^k$ , if  $SLS_i^k$  exists; otherwise  $A[i] = B[i] = \text{NIL}$ .
   Note that  $SUS_1^k = SLS_1^k = S[A[1]..B[1]]$ , which must be existing and has been
   computed.
   Next, we compute  $SUS_i^k$  for all  $i \geq 2$ . */

10 for  $i = 2 \dots n$  do
11   if  $A[i] = B[i] = \text{NIL}$  then
12      $A[i] \leftarrow A[i - 1]$ ;  $B[i] \leftarrow B[i - 1] + 1$ ;          //  $SUS_i^k = SUS_{i-1}^k S[i]$ 
13   else if  $B[i - 1] = i - 1$  and  $B[i - 1] - A[i - 1] + 2 < B[i] - A[i] + 1$  then
14      $A[i] \leftarrow A[i - 1]$ ;  $B[i] \leftarrow B[i - 1] + 1$ ;          //  $SUS_i^k = SUS_{i-1}^k S[i]$ 
15   /* Otherwise, do nothing.  $SUS_i^k = SLS_i^k$ . */
```
